



7 OIPE

RAW SEQUENCE LISTING

DATE: 02/07/2002

PATENT APPLICATION: US/09/935,726

TIME: 13:34:45

Input Set : A:\PF112P3D1C1subSL.txt

Output Set: N:\CRF3\02072002\I935726.raw

p.s

3 <110> APPLICANT: Hu, Jin-Shan
 4 Craig, Rosen
 5 Cao, Liang
 7 <120> TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
 9 <130> FILE REFERENCE: PF112P3D1C1
 11 <140> CURRENT APPLICATION NUMBER: 09/935,726
 12 <141> CURRENT FILING DATE: 2001-08-24
 14 <150> PRIOR APPLICATION NUMBER: 09/438,538
 15 <151> PRIOR FILING DATE: 1999-11-12
 17 <160> NUMBER OF SEQ ID NOS: 35
 19 <170> SOFTWARE: PatentIn version 3.0
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 24 <213> ORGANISM: Homo sapiens
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 44 Leu Ala Ala Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala
 45 -10 -5 -1 1 5
 47 gcc gcc ttc gag tcc gga ctc gac ctc tcg gac gcg gag ccc gac gcg 146
 48 Ala Ala Phe Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala
 49 10 15 20
 51 ggc gag gcc acg gct tat gca agc aaa gat ctg gag gag cag tta cgg 194
 52 Gly Glu Ala Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg
 53 25 30 35
 55 tct gtg tcc agt gta gat gaa ctc atg act gta ctc tac cca gaa tat 242
 56 Ser Val Ser Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr
 57 40 45 50
 59 tgg aaa atg tac aag tgt cag cta agg aaa gga ggc tgg caa cat aac 290
 60 Trp Lys Met Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn
 61 55 60 65 70

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64	Arg	Glu	Gln	Ala	Asn	Leu	Asn	Ser	Arg	Thr	Glu	Glu	Thr	Ile	Lys	Phe	
65				75					80					85			
67	gct	gca	gca	cat	tat	aat	aca	gag	atc	ttg	aaa	agt	att	gat	aat	gag	386
68	Ala	Ala	Ala	His	Tyr	Asn	Thr	Glu	Ile	Leu	Lys	Ser	Ile	Asp	Asn	Glu	
69				90					95					100			
71	tgg	aga	aag	act	caa	tgc	atg	cca	cgg	gag	gtg	tgt	ata	gat	gtg	ggg	434
72	Trp	Arg	Lys	Thr	Gln	Cys	Met	Pro	Arg	Glu	Val	Cys	Ile	Asp	Val	Gly	
73				105					110					115			
75	aag	gag	ttt	gga	gtc	gcg	aca	aac	acc	ttc	ttt	aaa	cct	cca	tgt	gtg	482
76	Lys	Glu	Phe	Gly	Val	Ala	Thr	Asn	Thr	Phe	Phe	Lys	Pro	Pro	Cys	Val	
77				120					125					130			
79	tcc	gtc	tac	aga	tgt	ggg	ggg	tgc	tgc	aat	agt	gag	ggg	ctg	cag	tgc	530
80	Ser	Val	Tyr	Arg	Cys	Gly	Gly	Cys	Cys	Asn	Ser	Glu	Gly	Leu	Gln	Cys	
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83	atg	aac	acc	agc	acg	agc	tac	ctc	agc	aag	acg	tta	ttt	gaa	att	aca	578
84	Met	Asn	Thr	Ser	Thr	Ser	Tyr	Leu	Ser	Lys	Thr	Leu	Phe	Glu	Ile	Thr	
85				155						160					165		
87	gtg	cct	ctc	tct	caa	ggc	ccc	aaa	cca	gta	aca	atc	agt	ttt	gcc	aat	626
88	Val	Pro	Leu	Ser	Gln	Gly	Pro	Lys	Pro	Val	Thr	Ile	Ser	Phe	Ala	Asn	
89				170						175					180		
91	cac	act	tcc	tgc	cga	tgc	atg	tct	aaa	ctg	gat	gtt	tac	aga	caa	gtt	674
92	His	Thr	Ser	Cys	Arg	Cys	Met	Ser	Lys	Leu	Asp	Val	Tyr	Arg	Gln	Val	
93				185					190					195			
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96	His	Ser	Ile	Ile	Arg	Arg	Ser	Leu	Pro	Ala	Thr	Leu	Pro	Gln	Cys	Gln	
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99	gca	gcg	aac	aag	acc	tgc	ccc	acc	aat	tac	atg	tgg	aat	aat	cac	atc	770
100	Ala	Ala	Asn	Lys	Thr	Cys	Pro	Thr	Asn	Tyr	Met	Trp	Asn	Asn	His	Ile	
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103	tgc	aga	tgc	ctg	gct	cag	gaa	gat	ttt	atg	ttt	tcc	tcg	gat	gct	gga	818
104	Cys	Arg	Cys	Leu	Ala	Gln	Glu	Asp	Phe	Met	Phe	Ser	Ser	Asp	Ala	Gly	
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107	gat	gac	tca	aca	gat	gga	ttc	cat	gac	atc	tgt	gga	cca	aac	aag	gag	866
108	Asp	Asp	Ser	Thr	Asp	Gly	Phe	His	Asp	Ile	Cys	Gly	Pro	Asn	Lys	Glu	
109				250						255					260		
111	ctg	gat	gaa	gag	acc	tgt	cag	tgt	gtc	tgc	aga	gcg	ggg	ctt	cgg	cct	914
112	Leu	Asp	Glu	Thr	Cys	Gln	Cys	Val	Cys	Arg	Ala	Gly	Leu	Arg	Pro		
113				265					270					275			
115	gcc	agc	tgt	gga	ccc	cac	aaa	gaa	cta	gac	aga	aac	tca	tgc	cag	tgt	962
116	Ala	Ser	Cys	Gly	Pro	His	Lys	Glu	Leu	Asp	Arg	Asn	Ser	Cys	Gln	Cys	
117				280					285					290			
119	gtc	tgt	aaa	aac	aaa	ctc	ttc	ccc	agc	caa	tgt	ggg	gcc	aac	cga	gaa	1010
120	Val	Cys	Lys	Asn	Lys	Leu	Phe	Pro	Ser	Gln	Cys	Gly	Ala	Asn	Arg	Glu	
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123	ttt	gat	gaa	aac	aca	tgc	cag	tgt	gta	tgt	aaa	aga	acc	tgc	ccc	aga	1058
124	Phe	Asp	Glu	Asn	Thr	Cys	Gln	Cys	Val	Cys	Lys	Arg	Thr	Cys	Pro	Arg	
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127	aat	caa	ccc	cta	aat	cct	gga	aaa	tgt	gcc	tgt	gaa	tgt	aca	gaa	agt	1106

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131 cca cag aaa tgc ttg tta aaa gga aag aag ttc cac cac caa aca tgc      1154
132 Pro Gln Lys Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys
133          345          350          355
135 agc tgt tac aga cgg cca tgt acg aac cgc cag aag gct tgt gag cca      1202
136 Ser Cys Tyr Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro
137          360          365          370
139 gga ttt tca tat agt gaa gaa gtg tgt cgt tgt gtc cct tca tat tgg      1250
140 Gly Phe Ser Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp
141 375          380          385          390
143 caa aga cca caa atg agc taagattgta ctgttttcca gttcatcgat      1298
144 Gln Arg Pro Gln Met Ser
145          395
147 tttctattat ggaaaactgt gttgccacag tagaactgtc tgtgaacaga gagacccttg      1358
149 tgggtocatg ctaacaaaga caaaagtctg tctttcctga accatgtgga taactttaca      1418
151 gaaatggact ggagctcatc tgcaaaaggc ctcttgtaaa gactggtttt ctgccaatga      1478
153 ccaaacagcc aagattttcc tcttggtgatt tctttaaaag aatgactata taattttattt      1538
155 ccactaaaaa tattgtttct gcattcattt ttatagcaac aacaattggg aaaactcact      1598
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185 Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
186          45          50          55
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190          60          65          70
193 Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
194          75          80          85
197 His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
198 90          95          100          105
201 Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
202          110          115          120
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206          125          130          135
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218 170      175      180      185
221 Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
222      190      195      200
225 Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
226      205      210      215
229 Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
230      220      225      230
233 Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
234      235      240      245
237 Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
238 250      255      260      265
241 Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
242      270      275      280
245 Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
246      285      290      295
249 Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
250      300      305      310
253 Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
254      315      320      325
257 Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
258 330      335      340      345
261 Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
262      350      355      360
265 Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
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287 <221> NAME/KEY: CDS

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298 Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys

299 -20

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305	ctc	aac	tca	agg	aca	gaa	gag	act	ata	aaa	ttt	gct	gca	gca	cat	tat	205
306	Leu	Asn	Ser	Arg	Thr	Glu	Glu	Thr	Ile	Lys	Phe	Ala	Ala	Ala	His	Tyr	
307				10					15						20		
309	aat	aca	gag	atc	ttg	aaa	agt	att	gat	aat	gag	tgg	aga	aag	act	caa	253
310	Asn	Thr	Glu	Ile	Leu	Lys	Ser	Ile	Asp	Asn	Glu	Trp	Arg	Lys	Thr	Gln	
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314	Cys	Met	Pro	Arg	Glu	Val	Cys	Ile	Asp	Val	Gly	Lys	Glu	Phe	Gly	Val	
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317	gcg	aca	aac	acc	ttc	ttt	aaa	cct	cca	tgt	gtg	tcc	gtc	tac	aga	tgt	349
318	Ala	Thr	Asn	Thr	Phe	Phe	Lys	Pro	Pro	Cys	Val	Ser	Val	Tyr	Arg	Cys	
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321	ggg	ggt	tgc	tgc	aat	agt	gag	ggg	ctg	cag	tgc	atg	aac	acc	agc	acg	397
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323	70				75					80					85		
325	agc	tac	ctc	agc	aag	acg	tta	ttt	gaa	att	aca	gtg	cct	ctc	tct	caa	445
326	Ser	Tyr	Leu	Ser	Lys	Thr	Leu	Phe	Glu	Ile	Thr	Val	Pro	Leu	Ser	Gln	
327				90					95					100			
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330	Gly	Pro	Lys	Pro	Val	Thr	Ile	Ser	Phe	Ala	Asn	His	Thr	Ser	Cys	Arg	
331				105					110					115			
333	tgc	atg	tct	aaa	ctg	gat	gtt	tac	aga	caa	gtt	cat	tcc	att	att	aga	541
334	Cys	Met	Ser	Lys	Leu	Asp	Val	Tyr	Arg	Gln	Val	His	Ser	Ile	Ile	Arg	
335				120				125					130				
337	cgt	tcc	ctg	cca	gca	aca	cta	cca	cag	tgt	cag	gca	gcg	aac	aag	acc	589
338	Arg	Ser	Leu	Pro	Ala	Thr	Leu	Pro	Gln	Cys	Gln	Ala	Ala	Asn	Lys	Thr	
339				135				140					145				
341	tgc	ccc	acc	aat	tac	atg	tgg	aat	aat	cac	atc	tgc	aga	tgc	ctg	gct	637
342	Cys	Pro	Thr	Asn	Tyr	Met	Trp	Asn	Asn	His	Ile	Cys	Arg	Cys	Leu	Ala	
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345	cag	gaa	gat	ttt	atg	ttt	tcc	tcg	gat	gct	gga	gat	gac	tca	aca	gat	685
346	Gln	Glu	Asp	Phe	Met	Phe	Ser	Ser	Asp	Ala	Gly	Asp	Asp	Ser	Thr	Asp	
347				170					175					180			
349	gga	ttc	cat	gac	atc	tgt	gga	cca	aac	aag	gag	ctg	gat	gaa	gag	acc	733
350	Gly	Phe	His	Asp	Ile	Cys	Gly	Pro	Asn	Lys	Glu	Leu	Asp	Glu	Glu	Thr	
351				185				190						195			
353	tgt	cag	tgt	gtc	tgc	aga	gcg	ggg	ctt	cgg	cct	gcc	agc	tgt	gga	ccc	781
354	Cys	Gln	Cys	Val	Cys	Arg	Ala	Gly	Leu	Arg	Pro	Ala	Ser	Cys	Gly	Pro	
355				200				205					210				
357	cac	aaa	gaa	cta	gac	aga	aac	tca	tgc	cag	tgt	gtc	tgt	aaa	aac	aaa	829
358	His	Lys	Glu	Leu	Asp	Arg	Asn	Ser	Cys	Gln	Cys	Val	Cys	Lys	Asn	Lys	
359				215				220					225				
361	ctc	ttc	ccc	agc	caa	tgt	ggg	gcc	aac	cga	gaa	ttt	gat	gaa	aac	aca	877
362	Leu	Phe	Pro	Ser	Gln	Cys	Gly	Ala	Asn	Arg	Glu	Phe	Asp	Glu	Asn	Thr	
363	230					235				240					245		
365	tgc	cag	tgt	gta	tgt	aaa	aga	acc	tgc	ccc	aga	aat	caa	ccc	cta	aat	925

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.



VERIFICATION SUMMARY

PATENT APPLICATION: US/09/935,726

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Input Set : A:\PF112P3D1C1subSL.txt

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L:687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8